



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

US/10/651,584

Source:

FEWO

Date Processed by STIC:

12/10/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/05/584

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ✓ Use of <220> Sequence(s) 1-20 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/651,584

DATE: 12/10/2003

TIME: 17:24:47

Input Set : A:\PTO.YF.asc

Output Set: N:\CRF4\12102003\J651584.raw

W--> 1 35
 3 <110> APPLICANT: Lauermann, Vit
 5 <120> TITLE OF INVENTION: Targeted release
 W--> 7 <130> FILE REFERENCE:
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/651,584
 11 <141> CURRENT FILING DATE: 2003-08-30
 13 <160> NUMBER OF SEQ ID NOS: 111

ERRORED SEQUENCES.

17 <210> SEQ ID NO: 1
 19 <211> LENGTH: 7
 E--> 21 <212> TYPE: peptide
 23 <213> ORGANISM: unknown
 W--> 26 <220> FEATURE:
 W--> 26 <223> OTHER INFORMATION:
 W--> 26 <400> 1
 28 SMSIARL
 32 <210> SEQ ID NO: 2
 34 <211> LENGTH: 13
 E--> 36 <212> TYPE: peptide
 38 <213> ORGANISM: unknown
 W--> 41 <220> FEATURE:
 W--> 41 <223> OTHER INFORMATION:
 W--> 41 <400> 2
 43 SKGSFSIQYT YHV
 47 <210> SEQ ID NO: 3
 49 <211> LENGTH: 13
 E--> 51 <212> TYPE: peptide
 53 <213> ORGANISM: unknown
 W--> 56 <220> FEATURE:
 W--> 56 <223> OTHER INFORMATION:
 W--> 56 <400> 3
 58 HLGGSQQLLH NKO
 62 <210> SEQ ID NO: 4
 64 <211> LENGTH: 14
 E--> 66 <212> TYPE: peptide
 68 <213> ORGANISM: unknown
 W--> 71 <220> FEATURE:
 W--> 71 <223> OTHER INFORMATION:
 W--> 71 <400> 4
 73 SKGKGTSQY SNTE

Use PRT, For a protein sequence.
 Does Not Comply
 Corrected Diskette Needed
 (P. 1-4)

Incomplete response,
 please see item 11, on error summary
 sheet.
 One letter amino acid designations
 are not to be used in a sequence.
 Please use 3 letter amino acids.

Same error

Same error

Same error

FYI: Number the amino acids under
 every five amino acids, do
 not use tab codes.

13 Please
 see Attached
 sample
 sequence
 listing format.

13

RAW SEQUENCE LISTING

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TIME: 17:24:47

Input Set : A:\PTO.YF.asc

Output Set: N:\CRF4\12102003\J651584.raw

77 <210> SEQ ID NO: 5
79 <211> LENGTH: 8
E--> 81 <212> TYPE: peptide
83 <213> ORGANISM: unknown
W--> 86 <220> FEATURE:
W--> 86 <223> OTHER INFORMATION:
W--> 86 <400> 5
88 DRVYIHPF 8
92 <210> SEQ ID NO: 6
94 <211> LENGTH: 12
E--> 96 <212> TYPE: peptide
98 <213> ORGANISM: unknown
W--> 101 <220> FEATURE:
W--> 101 <223> OTHER INFORMATION:
W--> 101 <400> 6
103 VVCGERGFFY TP 12
107 <210> SEQ ID NO: 7
109 <211> LENGTH: 7
E--> 111 <212> TYPE: peptide
113 <213> ORGANISM: unknown
W--> 116 <220> FEATURE:
W--> 116 <223> OTHER INFORMATION:
W--> 116 <400> 7
118 FFYTPKA 7
122 <210> SEQ ID NO: 8
124 <211> LENGTH: 9
E--> 126 <212> TYPE: peptide
128 <213> ORGANISM: unknown
W--> 131 <220> FEATURE:
W--> 131 <223> OTHER INFORMATION:
W--> 131 <400> 8
133 KRRPVKVYP 9
137 <210> SEQ ID NO: 9
139 <211> LENGTH: 12
E--> 141 <212> TYPE: peptide
143 <213> ORGANISM: unknown
W--> 146 <220> FEATURE:
W--> 146 <223> OTHER INFORMATION:
W--> 146 <400> 9
148 PVGKKRRPVK VY 12
152 <210> SEQ ID NO: 10
154 <211> LENGTH: 12
E--> 156 <212> TYPE: peptide
158 <213> ORGANISM: unknown
W--> 162 <220> FEATURE:
W--> 162 <223> OTHER INFORMATION:
W--> 162 <400> 10
164 KPVGKKRRPV KV 12
168 <210> SEQ ID NO: 11

Same error

Same error

Same error

Same error

Same error

Same error

RAW SEQUENCE LISTING

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TIME: 17:24:47

Input Set : A:\PTO.YF.asc

Output Set: N:\CRF4\12102003\J651584.raw

170 <211> LENGTH: 12
E--> 172 <212> TYPE: peptide
174 <213> ORGANISM: unknown
W--> 177 <220> FEATURE:
W--> 177 <223> OTHER INFORMATION:
W--> 177 <400> 11
179 GKPVGKKRRP VK
183 <210> SEQ ID NO: 12
185 <211> LENGTH: 13
E--> 187 <212> TYPE: peptide
189 <213> ORGANISM: unknown
W--> 192 <220> FEATURE:
W--> 192 <223> OTHER INFORMATION:
W--> 192 <400> 12
194 TFAGNAVRRS VGO
198 <210> SEQ ID NO: 13
200 <211> LENGTH: 6
E--> 202 <212> TYPE: peptide
204 <213> ORGANISM: unknown
W--> 207 <220> FEATURE:
W--> 207 <223> OTHER INFORMATION:
W--> 207 <400> 13
209 PLGLWA
213 <210> SEQ ID NO: 14
215 <211> LENGTH: 5
E--> 217 <212> TYPE: peptide
219 <213> ORGANISM: unknown
W--> 222 <220> FEATURE:
W--> 222 <223> OTHER INFORMATION:
W--> 222 <400> 14
224 PLFYS
228 <210> SEQ ID NO: 15
230 <211> LENGTH: 5
E--> 232 <212> TYPE: peptide
234 <213> ORGANISM: unknown
W--> 237 <220> FEATURE:
W--> 237 <223> OTHER INFORMATION:
W--> 237 <400> 15
239 PRTLTL
243 <210> SEQ ID NO: 16
245 <211> LENGTH: 5
E--> 247 <212> TYPE: peptide
249 <213> ORGANISM: unknown
W--> 252 <220> FEATURE:
W--> 252 <223> OTHER INFORMATION:
W--> 252 <400> 16
254 PERLS
258 <210> SEQ ID NO: 17
260 <211> LENGTH: 6

same error

12

same error

13

same error

6

same error

5

same error

5

same error

5

RAW SEQUENCE LISTING

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Input Set : A:\PTO.YF.asc

Output Set: N:\CRF4\12102003\J651584.raw

E--> 262 <212> TYPE: peptide
264 <213> ORGANISM: unknown
W--> 267 <220> FEATURE:
W--> 267 <223> OTHER INFORMATION:
W--> 267 <400> 17
269 HSSKLO
273 <210> SEQ ID NO: 18
275 <211> LENGTH: 6
E--> 277 <212> TYPE: peptide
279 <213> ORGANISM: unknown
W--> 282 <220> FEATURE:
W--> 282 <223> OTHER INFORMATION:
W--> 282 <400> 18
284 SQYSNT
288 <210> SEQ ID NO: 19
290 <211> LENGTH: 7
E--> 292 <212> TYPE: peptide
294 <213> ORGANISM: unknown
W--> 297 <220> FEATURE:
W--> 297 <223> OTHER INFORMATION:
W--> 297 <400> 19
299 QFYSSNK
303 <210> SEQ ID NO: 20
305 <211> LENGTH: 12
E--> 307 <212> TYPE: peptide
309 <213> ORGANISM: unknown
W--> 312 <220> FEATURE:
W--> 312 <223> OTHER INFORMATION:
W--> 312 <400> 20
314 VSQNYPIVQN FN

Same error

Same error

Same error

Same error

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\PTO.YF.asc

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Use of <220> Feature (NEW RULES): *Error explanation*

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)

(Sec.1.823 of new Rules)

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27

Seq#:28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51

Seq#:52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75

Seq#:76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99

Seq#:100,101,102,103,104,105,106,107,108,109,110,111

VERIFICATION SUMMARY

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Input Set : A:\PTO.YF.asc

Output Set: N:\CRF4\12102003\J651584.raw

L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:7 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:21 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:26 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:1, <213>
ORGANISM:unknown
L:26 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>
ORGANISM:unknown
L:26 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:26
L:36 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:41 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>
ORGANISM:unknown
L:41 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
ORGANISM:unknown
L:41 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:41
L:51 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:56 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:3, <213>
ORGANISM:unknown
L:56 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>
ORGANISM:unknown
L:56 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:56
L:66 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:71 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213>
ORGANISM:unknown
L:71 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
ORGANISM:unknown
L:71 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:71
L:81 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:86 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>
ORGANISM:unknown
L:86 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:unknown
L:86 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:86
L:96 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:101 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>
ORGANISM:unknown
L:101 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:unknown
L:101 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:101
L:111 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:116 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213>
ORGANISM:unknown
L:116 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>
ORGANISM:unknown
L:116 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:116
L:126 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:131 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>
ORGANISM:unknown
L:131 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:unknown
L:131 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:131
L:141 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:146 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:9, <213>

ORGANISM:unknown
L:146 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>
ORGANISM:unknown
L:146 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:146
L:156 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:162 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>
ORGANISM:unknown
L:162 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:unknown
L:162 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:162
L:172 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:177 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:11, <213>
ORGANISM:unknown
L:177 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>
ORGANISM:unknown
L:177 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:177
L:187 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

VERIFICATION SUMMARY

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TIME: 17:24:48

Input Set : A:\PTO.YF.asc

Output Set: N:\CRF4\12102003\J651584.raw

L:192 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:12, <213>
ORGANISM:unknown
L:192 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>
ORGANISM:unknown
L:192 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:192
L:202 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:207 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:13, <213>
ORGANISM:unknown
L:207 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:13, <213>
ORGANISM:unknown
L:207 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:207
L:217 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:222 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:14, <213>
ORGANISM:unknown
L:222 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>
ORGANISM:unknown
L:222 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:222
L:232 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:237 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:15, <213>
ORGANISM:unknown
L:237 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213>
ORGANISM:unknown
L:237 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:237
L:247 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:252 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:16, <213>
ORGANISM:unknown
L:252 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:16, <213>
ORGANISM:unknown
L:252 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:252
L:262 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:267 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:17, <213>
ORGANISM:unknown
L:267 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:17, <213>
ORGANISM:unknown
L:277 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:292 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:307 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:322 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:337 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:352 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:367 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:382 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:397 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:412 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:427 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:442 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:457 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:472 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:487 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:502 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:517 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:532 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:547 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

L:563 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:578 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:593 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:608 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:623 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:638 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:653 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:668 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

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Input Set : A:\PTO.YF.asc

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L:683 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:698 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:713 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:728 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:743 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:758 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

<110> Smith, John; Smithgene Inc.

<120> Example of a Sequence Listing

<130> 01-00001

<140> PCT/EP98/00001

<141> 1998-12-31

<150> US 08/999,999

<151> 1997-10-15

<160>

<170> PatentIn version 2.0

<210>

1

<211>

389

<212>

DNA

<213>

Paramecium sp.

<220>

<221>

CDS

<222>

(279)...(389)

<300>

<301>

Doc. Richard

<302>

Isolation and Characterization of a Gene Encoding a
Protease from Paramecium sp.

<303>

Journal of Genes

<304>

1

<305>

4

<306>

1-7

<307>

1988-06-31

<308>

123456

<309>

1988-06-31

<400>

1

agctgtatgc attcctgtgt cctcttctct ctgggcttct caccctgtca atcagatctc

60

agggagagtg tcttgacctt cctctgcctt tgcagcttca caggcaggca ggcaggcagc

120

tgatgtggca attgctggca gtgccacagg ctttccagcc aggccttaggg tgggttccgc

180

cgcggcgagg cggccctctt cgcgtctctc tcgcgcctct ctctcgtctt cctctcgtct

240

Appendix 3, page 2

ggacctgatt aggtgagcag gaggaggggg cagttagc 290
Met Val Ser Met Phe Ser

ttg tct ttc aaa tgg cct gga ttt tgt ttg bct gtt tgt ttg ttc caa 300
Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu Phe Val Cys Leu Phe Gln

tgt ccc aaa gtc ctc ccc tgt cac tca tca ctg cag ccg aat ctt 389
Cys Pro Lys Val Leu Pro Cys His Ser Ser Leu Gln Pro Asn Leu

<210> 2
<211> 37
<212> PRT
<213> Paramecium sp.

<400> 2
Met Val Ser Met Phe Ser Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu
1 5 10 15

Phe Val Cys Leu Phe Gln Cys Pro Lys Val Leu Pro Cys His Ser Ser
20 25 30

Leu Gln Pro Asn Leu
35

<210>)
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> Designed peptide based on size and polarity to act as a linker between the alpha and beta chains of Protein XYZ.

<400>)
Met Val Asn Leu Glu Pro Met His Thr Glu Ile
1 5 10

<210> 4
<400> 4
000

[Annex VIII follows]

Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M, when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO: #:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

cule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.

<213>

Organism

Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.

<220>

Feature

Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.

M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.

<221>

Name/Key

Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6

M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence

<222>

Location

Specify location within sequence; where appropriate state number of first and last bases/amino acids

M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified

<223>	Other Information	Other relevant information; four lines maximum	0	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	0	
<301>	Authors	Preferably max. of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	0	
<302>	Title		0	
<303>	Journal		0	
<304>	Volume		0	
<305>	Issue		0	
<306>	Pages		0	
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, 1001-yyyy or Season-yyyy	0	
<308>	Database Accession Number	Accession number assigned by database including database name	0	
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or 1001-yyyy	0	
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	0	

type citations only;
specify as yyyy-mm-dd

<312>

Publication Date

Document publication
date, for
patent-type
citations only;
specify as yyyy-mm-dd

0

<313>

Relevant
Residues

FROM (position) TO
(position)

0

<400>

Sequence

SEQ ID NO should
follow the
numeric identifier
and should appear
on the line pre-
ceding the actual
sequence

M

5. Section 1.024 is revised to read as follows:

1.024 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.021(c) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer-readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;

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